

## SEQUENCE LISTING

<110> Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of  
Flavivirus Infection

<130> 14114.0332U3

<150> PCT/US99/12298

<151> 1999-06-03

<150> 09/701,536

<151> 2000-11-29

<150> 60/087,908

<151> 1998-06-04

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Description of artificial sequence; note =  
synthetic construct

<221> CDS

<222> (25) ... (48)

<221> misc\_feature

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<223> Amplimer 14DV389

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Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro		
225 230 235		
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Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu		
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Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val		
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Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn		
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Gly Cys Gly Leu Phe Gly Lys Ser Ile Asp Thr Cys Ala Lys Phe		
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Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile		
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Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn		
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Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg		
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Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr			
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Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His			
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cag gct ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag			2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys			
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Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu			
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Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln			
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Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe			
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Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr			
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Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys			
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<223> pCDJE 2-7

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Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp  
35 40 45  
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys  
50 55 60  
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
65 70 75 80  
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
85 90 95  
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
100 105 110  
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
115 120 125  
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
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Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
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Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val  
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Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
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Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
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Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
225 230 235 240  
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
245 250 255  
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
260 265 270  
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val  
275 280 285  
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu  
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Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
305 310 315 320  
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
325 330 335  
Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr  
340 345 350  
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
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370 375 380  
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<221> misc\_feature  
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 Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys  
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335 340 345	
gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct	2005
Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro	
350 355 360 365	
tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt	2053

Ser	Tyr	Thr	Leu	Lys	Leu	Gly	Glu	Tyr	Gly	Glu	Val	Thr	Val	Asp	Cys	
			370			375					380					
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt															2101	
Glu	Pro	Arg	Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val	
			385			390					395					
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac															2149	
Gly	Thr	Lys	Thr	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	Met	Asp	Leu	Asn	
			400			405					410					
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg															2197	
Leu	Pro	Trp	Ser	Ser	Ala	Gly	Ser	Thr	Val	Trp	Arg	Asn	Arg	Glu	Thr	
			415			420					425					
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca															2245	
Leu	Met	Glu	Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Ser	Val	Ile	Ala	
			430			435					440			445		
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att															2293	
Leu	Gly	Ser	Gln	Glu	Gly	Ala	Leu	His	Gln	Ala	Leu	Ala	Gly	Ala	Ile	
			450			455					460					
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg															2341	
Pro	Val	Glu	Phe	Ser	Ser	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	His	Leu	
			465			470					475					
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat															2389	
Lys	Cys	Arg	Val	Lys	Met	Glu	Lys	Leu	Gln	Leu	Lys	Gly	Thr	Thr	Tyr	
			480			485					490					
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca															2437	
Gly	Val	Cys	Ser	Lys	Ala	Phe	Lys	Phe	Leu	Gly	Thr	Pro	Ala	Asp	Thr	
			495			500					505					
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga															2485	
Gly	His	Gly	Thr	Val	Val	Leu	Glu	Leu	Gln	Tyr	Thr	Gly	Thr	Asp	Gly	
			510			515					520			525		
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg															2533	
Pro	Cys	Lys	Val	Pro	Ile	Ser	Ser	Val	Ala	Ser	Leu	Asn	Asp	Leu	Thr	
			530			535					540					
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg															2581	
Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ser	Val	Ala	Thr	
			545			550					555					
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca															2629	
Ala	Asn	Ala	Lys	Val	Leu	Ile	Glu	Leu	Glu	Pro	Pro	Phe	Gly	Asp	Ser	
			560			565					570					
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac															2677	
Tyr	Ile	Val	Val	Gly	Arg	Gly	Glu	Gln	Gln	Ile	Asn	His	His	Trp	His	
			575			580					585					

aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga	2725
Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly	
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gct cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca	2773
Ala Gln Arg Leu Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser	
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gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc	2821
Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe	
625 630 635	
gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa	2869
Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln	
640 645 650	
gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat	2917
Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp	
655 660 665	
agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc	2965
Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe	
670 675 680 685	
ctc tcc gtg aac gtg cac gcc t gaaggccggcc gctcgagcat gcatctagag	3017
Leu Ser Val Asn Val His Ala	
690	
ggccctattc tatagtgtca cctaaatgct agagctcgct gatcaggcctc gactgtgcct	3077
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tgtcattctta ttctgggggg tgggggtgggg caggacagca agggggagga ttgggaagac	3257
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gattatcaaa aaggatctt acctagatcc tttaaaatataaaaatgaaat tttaaatcaa	4277
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ctatctcaggc gatctgtctt tttcggttcat ccatacgatgc ctgactcccc gtcgtgtaga	4397
taactacgat acgggaggccc ttaccatctg gcccaggatgc tgcaatgata cccgcgagacc	4457
cacgctcacc ggctccagat ttatcagcaaa taaaaccagcc agccggaaagg gcccggcgca	4517

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gagttacatg	atccccatg	ttgtcaaaa	aagcggttag	ctccttcggt	cctccgatcg	4757
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ctcttactgt	catgcacatcc	gtaagatgct	tttctgtgac	tggttagtac	tcaaccaagt	4877
cattctgaga	atagtgtatg	cggcgaccga	gttgcgttgc	cccgccgtca	atacgggata	4937
ataccgcgcc	acatagcaga	actttaaaag	tgctcatcat	tggaaaacgt	tcttcggggc	4997
gaaaactctc	aaggatcttta	ccgctgttga	gatccagttc	gatgtAACCC	actcgtgcac	5057
ccaaactgatc	ttcagcatct	tttactttca	ccagcgtttc	tgggtgagca	aaaacaggaa	5117
ggcaaaatgc	cgcaaaaaag	ggaataaggg	cgacacggaa	atgttgaata	ctcataactct	5177
tccttttca	atattattga	agcatttatac	agggttatttgc	tctcatgagc	ggatacatat	5237
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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<223> pCBWN

<400> 16

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Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Val	Thr	Leu	Ser	Asn	Phe	Gln	Gly
									20			25			30
Lys	Val	Met	Met	Thr	Val	Asn	Ala	Thr	Asp	Val	Thr	Asp	Val	Ile	Thr
									35			40			45
Ile	Pro	Thr	Ala	Ala	Gly	Lys	Asn	Leu	Cys	Ile	Val	Arg	Ala	Met	Asp
									50			55			60
Val	Gly	Tyr	Met	Cys	Asp	Asp	Thr	Ile	Thr	Tyr	Glu	Cys	Pro	Val	Leu
									65			70			75
Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Thr	Lys	Ser
									85			90			95
Ala	Val	Tyr	Val	Arg	Tyr	Gly	Arg	Cys	Thr	Lys	Thr	Arg	His	Ser	Arg
									100			105			110
Arg	Ser	Arg	Arg	Ser	Leu	Thr	Val	Gln	Thr	His	Gly	Glu	Ser	Thr	Leu
									115			120			125
Ala	Asn	Lys	Lys	Gly	Ala	Trp	Met	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr
									130			135			140
Leu	Val	Lys	Thr	Glu	Ser	Trp	Ile	Leu	Arg	Asn	Pro	Gly	Tyr	Ala	Leu
									145			150			155
Val	Ala	Ala	Val	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Thr	Met	Gln	Arg
									165			170			175
Val	Val	Phe	Val	Val	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	
									180			185			190
Asn	Cys	Leu	Gly	Met	Ser	Asn	Arg	Asp	Phe	Leu	Glu	Gly	Val	Ser	Gly
									195			200			205

Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile  
 210 215 220  
 Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu  
 225 230 235 240  
 Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val  
 245 250 255  
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His  
 260 265 270  
 Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val  
 275 280 285  
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
 290 295 300  
 Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr  
 305 310 315 320  
 Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
 325 330 335  
 Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala  
 340 345 350  
 Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr  
 355 360 365  
 Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg  
 370 375 380  
 Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys  
 385 390 395 400  
 Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp  
 405 410 415  
 Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu  
 420 425 430  
 Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser  
 435 440 445  
 Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu  
 450 455 460  
 Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg  
 465 470 475 480  
 Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys  
 485 490 495  
 Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly  
 500 505 510  
 Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys  
 515 520 525  
 Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly  
 530 535 540  
 Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala  
 545 550 555 560  
 Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 565 570 575  
 Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly  
 580 585 590  
 Ser Ser Ile Gly Lys Ala Phe Thr Thr Leu Lys Gly Ala Gln Arg  
 595 600 605  
 Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly  
 610 615 620  
 Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
 645 650 655  
 Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile  
 660 665 670  
 Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val  
 675 680 685  
 Asn Val His Ala  
 690

<210> 17  
 <211> 5334  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<221> CDS  
 <222> (916) ... (3007)  
 <221> misc\_feature  
 <222> (1) ... (5334)  
 <223> pCBJE 1-14

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 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggagggtcgct gagtagtgcg 120  
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180  
 ttagggtag gcgtttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240  
 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agccatata 300  
 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360  
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420  
 attgacgtca atgggtggag tatttacggt aaactgccc cttggcagta catcaagtgt 480  
 atcatatgccc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540  
 atgcccagta catgaccccta tgggactttc ctacttggca gtacatctac gtattagtca 600  
 tcgctattac catggtgatg cgggtttggc agtacatcaa tggcgtgga tagcggtttg 660  
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttggcacc 720  
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780  
 gtaggcgtgt acgggtggag gtctatataa gcagagctct ctggctact agagaaccca 840  
 ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc 900  
 tctagagccg cgcgc atg ggc aga aag caa aac aaa aga gga gga aat gaa 951  
 Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu  
 1 5 10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg 999  
 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala  
 15 20 25

gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc 1047  
 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile  
 30 35 40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	45	50	55	60	1095
gag aac aga tgc tgg gtc cg <sup>g</sup> gca atc gac gtc ggc tac atg tgt gag Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	65	70	75		1143
gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	80	85	90		1191
gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	95	100	105		1239
gga cg <sup>g</sup> tgc acg cg <sup>g</sup> acc agg cat tcc aag cga agc agg aga tcc gtg Gly Arg Cys Thr Arg Thr His Ser Lys Arg Ser Arg Arg Ser Val	110	115	120		1287
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	125	130	135	140	1335
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	145	150	155		1383
tgg atc ata agg aat cct ggc tat gct ttc ctg gcg gcg gta ctt ggc Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	160	165	170		1431
tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu	175	180	185		1479
ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly	190	195	200		1527
aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu	205	210	215	220	1575
gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro	225	230	235		1623
aca ttg gac gtc cg <sup>g</sup> atg att aac atc gaa gct agc caa ctt gct gag Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu	240	245	250		1671
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg					1719

Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val			
255	260	265	
gct cggtgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat			1767
Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp			
270	275	280	
agt agc tat gtgtgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac			1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn			
285	290	295	300
gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc			1863
Gly Cys Gly Leu Phe Gly Lys Ser Ile Asp Thr Cys Ala Lys Phe			
305	310	315	
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc			1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile			
320	325	330	
aaa tac gaa gtt ggc att ttt gtgtcat gga acc acc act tcg gaa aac			1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn			
335	340	345	
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt			2007
His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe			
350	355	360	
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac			2055
Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr			
365	370	375	380
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa			2103
Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu			
385	390	395	
gcgttt tac gtc atg acc gtgg tca aag tca ttt ctg gtc cat agg			2151
Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg			
400	405	410	
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca			2199
Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr			
415	420	425	
gcgtgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc			2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala			
430	435	440	
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat			2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Leu His			
445	450	455	460
cag gcg ttg gca gga gcc atc gtgtgtg gag tac tca agc tca gtg aag			2343
Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys			
465	470	475	

tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala 480	485	490	2391	
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495	500	505	2439	
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510	515	520	2487	
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525	530	535	540	2535
agc ctc aat gac atg acc ccc gtt ggg cg <sup>g</sup> ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545	550	555	2583	
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu 560	565	570	2631	
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln 575	580	585	2679	
atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe 590	595	600	2727	
tca aca act ttg aag gga gct caa aga ctg gca gc <sup>g</sup> ttg ggc gac aca Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr 605	610	615	620	2775
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625	630	635	2823	
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640	645	650	2871	
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met 655	660	665	2919	
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr 670	675	680	2967	
ggg ggt gtg ctc gtg ttc tta gc <sup>g</sup> acc aat gtg cat gct t aattagttg			3017	

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala  
 685 690 695

agcggccgct cgagcatgca tctagagggc cctattctat agtgtcacct aaatgctaga 3077  
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 cacggaaatg ttgaataactc atactcttcc ttttcaata ttattgaagc atttatcagg 5237  
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<210> 18  
 <211> 697  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<223> pCBJE 1-14

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 20 25 30  
 Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp  
 35 40 45  
 Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys  
 50 55 60  
 Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr  
 65 70 75 80  
 Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp  
 85 90 95  
 Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr  
 100 105 110  
 Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr  
 115 120 125  
 His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser  
 130 135 140  
 Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg  
 145 150 155 160  
 Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly  
 165 170 175  
 Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val  
 180 185 190  
 Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe  
 195 200 205  
 Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly  
 210 215 220  
 Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val  
 225 230 235 240  
 Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr  
 245 250 255  
 Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro  
 260 265 270  
 Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val  
 275 280 285  
 Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu  
 290 295 300  
 Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser  
 305 310 315 320  
 Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val  
 325 330 335  
 Gly Ile Phe Val His Gly Thr Thr Ser Glu Asn His Gly Asn Tyr  
 340 345 350  
 Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro  
 355 360 365  
 Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr  
 370 375 380  
 Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val  
 385 390 395 400  
 Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His  
 405 410 415

Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	Ala	Trp	Arg	Asn
				420				425					430		
Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	Thr	Lys	Gln	Ser
				435			440					445			
Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	Gln	Ala	Leu	Ala
				450			455				460				
Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	Leu	Thr	Ser	Gly
				465			470				475				480
His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	Leu	Lys	Gly	Thr
					485				490					495	
Thr	Tyr	Gly	Met	Cys	Thr	Glu	Lys	Phe	Ser	Phe	Ala	Lys	Asn	Pro	Ala
					500			505					510		
Asp	Thr	Gly	His	Gly	Thr	Val	Val	Ile	Glu	Leu	Ser	Tyr	Ser	Gly	Ser
					515			520				525			
Asp	Gly	Pro	Cys	Lys	Ile	Pro	Ile	Ala	Ser	Val	Ala	Ser	Leu	Asn	Asp
					530			535				540			
Met	Thr	Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ala	Thr
					545			550				555			560
Ser	Ser	Ala	Ser	Ser	Lys	Val	Leu	Val	Glu	Met	Glu	Pro	Pro	Phe	Gly
						565			570					575	
Asp	Ser	Tyr	Ile	Val	Val	Gly	Arg	Gly	Asp	Lys	Gln	Ile	Asn	His	His
					580			585				590			
Trp	His	Lys	Ala	Gly	Ser	Thr	Leu	Gly	Lys	Ala	Phe	Ser	Thr	Thr	Leu
						595		600				605			
Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe
						610		615				620			
Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile	Gly	Lys	Ala	Val	His	Gln
						625		630			635				640
Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile
							645			650				655	
Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Val	Asn	Ala
							660			665				670	
Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr	Gly	Gly	Val	Leu
							675			680				685	
Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala							
					690			695							

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<210> 19
<211> 5283
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> CDS  
<222> (910) . . . (2965)

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ccgcatagtt  aagccagtt  ctgctccctg  cttgtgtgtt  ggaggtcgct  gagtagtgcg  120
cgagcaaaat  ttaagctaca  acaaggcaag  gcttgaccga  caattgcatt  aagaatctgc  180
tttagggttag  qcqtttqcg  ctqcttcqcg  atqtagggc  cagatataacg  cgttgacatt  240
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gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300  
 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360  
 cccgcccatt gacgtcaata atgacgtatg ttccatagt aacgccaata gggactttcc 420  
 attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt 480  
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540  
 atgcccagta catgacccta tgggactttc ctacttggca gtacatctac gtattagtca 600  
 tcgctattac catggtgatg cggtttggc agtacatcaa tgggctgga tagcggtttg 660  
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttgc tttggcacc 720  
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatggcgg 780  
 gtaggcgtgt acggtggag gtctatataa gcagagctct ctggctaact agagaacccaa 840  
 ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc 900  
 gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951  
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cggttggc gac 999  
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp  
 15 20 25 30

agg gaa gga tac atg gtt atg cggtttggc agt gga agg gac gct gca agc 1047  
 Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser  
 35 40 45

cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg 1095  
 Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met  
 50 55 60

gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac 1143  
 Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp  
 65 70 75

cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat 1191  
 Gln Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp  
 80 85 90

agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg 1239  
 Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg  
 95 100 105 110

ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc 1287  
 Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val  
 115 120 125

ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc 1335  
 Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val  
 130 135 140

acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc 1383  
 Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala  
 145 150 155

att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg 1431  
 Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val  
 160 165 170

act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg	1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg	
175 180 185 190	
tgc acg cat ctt gag aac aga gat ttt gtg aca gga actcaa ggg acc	1527
Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr	
195 200 205	
acc aga gtg tcc cta gtt ttg gaa ctt gga ggc tgc gtg acc atc aca	1575
Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr	
210 215 220	
gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag	1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln	
225 230 235	
gaa agc ccg gct gaa acc aga gaa tac tgc ctg cac gcc aaa ttg acc	1671
Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr	
240 245 250	
aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt	1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu	
255 260 265 270	
ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac	1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp	
275 280 285	
cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg	1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac	1863
Ala Cys Ala Lys Phe Glu Cys Glu Ala Lys Lys Ala Val Gly His	
305 310 315	
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac	1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His	
320 325 330	
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca	1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser	
335 340 345 350	
gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac	2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp	
355 360 365	
tat gga gat gtg tcg acg tgt aaa gtg gca agt ggg att gat gtc	2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val	
370 375 380	
gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct	2103

Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro			
385	390	395	
tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc			2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro			
400	405	410	
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg			2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val			
415	420	425	430
gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg			2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly			
435	440	445	
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc			2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala			
450	455	460	
agt gtg gag ggc cag aaa tac cac ctg aaa agc ggc cat gtt act tgt			2343
Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys			
465	470	475	
gat gtg gga ctg gaa aag ctg aaa ggc aca acc tac tcc atg			2391
Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met			
480	485	490	
tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc			2439
Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly			
495	500	505	510
cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca			2487
His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro			
515	520	525	
tgt cgg atc ccc gtg cgg gct gtg gca cat ggt gtc cca gcg gtt aat			2535
Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn			
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gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc			2583
Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly			
545	550	555	
gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg			2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val			
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gga gac ctt agc cag cag tgg ttt cag aaa ggc agt acc att ggt aga			2679
Gly Asp Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg			
575	580	585	590
atg ttt gaa aaa acc cgc agg gga ttg gaa agg ctc tct gtg gtt gga			2727
Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly			
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Glu His Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val	
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620	
ggg aag gca atc cac acg gtg ctg ggg gga gct ttc aac acc ctt ttt	2823
Gly Lys Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe	
625	630
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ggg ggg gtt gga ttc atc cct aag atg ctg ctg ggg gtt gct ctg gtc	2871
Gly Gly Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val	
640	645
650	
tgg ttg gga cta aat gcc agg aat cca acg atg tcc atg acg ttt ctt	2919
Trp Leu Gly Leu Asn Ala Arg Asn Pro Thr Met Ser Met Thr Phe Leu	
655	660
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670	
gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca t	2965
Ala Val Gly Ala Leu Thr Leu Met Met Thr Met Gly Val Gly Ala	
675	680
685	
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tcatcattgg	aaaacgttct	tcggggcgaa	aactctcaag	gatcttaccg	ctgtttagat	5005
ccagttcgat	gtaacccact	cgtgcaccca	actgatcttc	agcatcttt	actttcacca	5065
gcgtttctgg	gtgagcaaaa	acaggaaggc	aaaatgccgc	aaaaaaaggga	ataagggcga	5125
cacggaaatg	ttgaataactc	atactcttcc	ttttcaata	ttattgaagc	atttatcagg	5185
gttattgtct	catgagcgg	tacatatttgc	aatgtattta	gaaaaataaa	caaatagggg	5245
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<210> 20

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<400> 20

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Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Val	Thr	Leu	Val	Arg	Lys	Asn	Arg
									20		25				30
Trp	Leu	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Phe	Ser
								35		40				45	
Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp
								50		55				60	
Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu
					65			70		75				80	
Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
					85			90						95	
Val	Ala	Tyr	Gly	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg	
					100			105						110	
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
					115			120						125	
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys
					130			135						140	
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu
					145			150		155				160	
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
					165			170						175	
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile
					180			185						190	
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
					195			200						205	
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
					210			215						220	
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
					225			230		235				240	
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
					245			250						255	
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
					260			265						270	
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
					275			280						285	

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys  
 290 295 300  
 Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln  
 305 310 315 320  
 Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys  
 325 330 335  
 Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu  
 340 345 350  
 Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu  
 355 360 365  
 Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala  
 370 375 380  
 Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp  
 385 390 395 400  
 Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met  
 405 410 415  
 His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val  
 420 425 430  
 Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly  
 435 440 445  
 Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu  
 450 455 460  
 His Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu  
 465 470 475 480  
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys  
 485 490 495  
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val  
 500 505 510  
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu  
 515 520 525  
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala  
 530 535 540  
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly  
 545 550 555 560  
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln  
 565 570 575  
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met  
 580 585 590  
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe  
 595 600 605  
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr  
 610 615 620  
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile  
 625 630 635 640  
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr  
 645 650 655  
 Arg Asn Met Thr Met Ser Met Ser Ile Leu Val Gly Val Ile Met  
 660 665 670  
 Met Phe Leu Ser Leu Gly Val Gly Ala  
 675 680

<210> 21  
 <211> 5304  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<221> CDS

<222> (910) ... (2986)

<400> 21

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ccgcatagtt	aagccagtat	ctgctccctg	cttgcgtgtt	ggagggtcgct	gagtagtgcg	120
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttagggtag	gcgtttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacgggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccgcc	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggac	tatttacggt	aaactgccc	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgcccagta	catgaccta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgcttattac	catggtgatg	cgggtttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
actcacgggg	atttccaagt	ctccacccca	ttgacgtcaa	tgggagtttgc	tttggcacc	720
aaaatcaacg	ggactttcca	aaatgtcgta	acaactccgc	cccatggacg	caaatggcgc	780
gtaggcgtgt	acgggtggag	gtctatataa	gcagagctct	ctggctact	agagaacccaa	840
ctgcttactg	gcttatcgaa	attaatacga	ctcaactatag	ggagacccaa	gcttggtacc	900
gccggccccc	atg ggc	aag agg	tcc gcc	gac tca	atc atg tgg ctc	951

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser

1 5 10

ttg gca gtt gtc	ata gct ggt	aca agc gct	ttg cag tta	tca acc tat	999
Leu Ala Val Val	Ile Ala Gly	Thr Ser Ala	Leu Gln	Leu Ser Thr	Tyr
15	20	25	30		

cag ggg aaa gtg tta	atg tca atc aac	aag act gac gct	caa agc gcc	1047
Gln Gly Lys Val	Leu Met Ser Ile	Asn Lys Thr	Asp Ala Gln	Ser Ala
35	40	45		

ata aac att cct	agt gcc aac gga	gca aac act tgc	att gtg agg gct	1095
Ile Asn Ile Pro	Ser Ala Asn Gly	Ala Asn Thr Cys	Ile Val Arg Ala	
50	55	60		

cta gat gtg ggg gtc	atg tgc aaa gat	gac atc aca tac	ctg tgc cca	1143
Leu Asp Val Gly	Val Met Cys Lys	Asp Asp Ile	Thr Tyr Leu Cys Pro	
65	70	75		

gtg ctt tca gcg gga	aat gat ccc gag	gac att gac tgc	tgt tgg tgc	1191
Val Leu Ser Ala	Gly Asn Asp Pro	Glu Asp Ile	Asp Cys Trp Cys Asp	
80	85	90		

gtc gaa gag gtg tgg	gtg cac tac ggc	aga tgc acg	cgcc atg gga	cat	1239
Val Glu Glu Val	Trp Val His	Tyr Gly Arg	Cys Thr Arg	Met Gly His	
95	100	105	110		

tcg agg cgt agc	cga cgg tca	atc tct	gtg cag	cat cat	gga gat tcc	1287
-----------------	-------------	---------	---------	---------	-------------	------

Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser  
 115 120 125  
 aca ctg gca aca aag aac acg cca tgg ttg gac acc gtc aaa acc acc acc 1335  
 Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr  
 130 135 140  
 aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat 1383  
 Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr  
 145 150 155  
 gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca 1431  
 Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr  
 160 165 170  
 cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac 1479  
 Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr  
 175 180 185 190  
 agc ttc aac tgt ctg gga aca tca aac agg gac ttt gtc gag gga gcc 1527  
 Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala  
 195 200 205  
 agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc 1575  
 Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val  
 210 215 220  
 aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag 1623  
 Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys  
 225 230 235  
 atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca 1671  
 Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala  
 240 245 250  
 acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa 1719  
 Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu  
 255 260 265 270  
 gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat 1767  
 Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp  
 275 280 285  
 gtt gtg gac cgc gga tgg ggt aac gga tgt ggt ctg ttt gga aaa ggg 1815  
 Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly  
 290 295 300  
 agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg 1863  
 Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly  
 305 310 315  
 aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg 1911  
 Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val  
 320 325 330

cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att		1959
His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile		
335 340 345 350		
gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc		2007
Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser		
355 360 365		
ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa		2055
Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu		
370 375 380		
gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag		2103
Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys		
385 390 395		
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt		2151
Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu		
400 405 410		
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg		2199
Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu		
415 420 425 430		
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta		2247
Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu		
435 440 445		
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca		2295
Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro		
450 455 460		
gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa		2343
Ala Thr Val Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys		
465 470 475		
tgc aga gct aag ctt gac aag gtc aaa atc aag gga acg aca tat ggc		2391
Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly		
480 485 490		
atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg		2439
Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly		
495 500 505 510		
cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc		2487
His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro		
515 520 525		
tgc cga gtt ccc atc tcc gtg act gca aac ctc atg gat ttg aca ccg		2535
Cys Arg Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro		
530 535 540		
gtt gga aga ttg gtc acg gtc aat ccc ttt ata agc aca ggg gga gcg		2583

Val Gly Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala		
545	550	555
aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac		2631
Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr		
560	565	570
atc gtc gtc gga aga ggc acc acc cag att aac tac cac tgg cac aaa		2679
Ile Val Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys		
575	580	585
gag gga agc agc att ggg aag gct ttg gcg acc aca tgg aaa gga gcc		2727
Glu Gly Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala		
595	600	605
caa cgg cta gcc gtc tta ggg gac aca gcg tgg gac ttt gga tct att		2775
Gln Arg Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile		
610	615	620
gga gga gtt ttc aat tca att ggc aaa gct gtc cac caa gtt ttc gga		2823
Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly		
625	630	635
gga gcg ttc agg act ctg ttc ggg gga atg tcc tgg atc aca cag ggg		2871
Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly		
640	645	650
cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg		2919
Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg		
655	660	665
670		
agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg		2967
Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu		
675	680	685
gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg		3016
Ala Thr Ser Val Gln Ala		
690		
ccctattctta tagtgtcacc taaatgctag agctcgctga tcagcctcga ctgtgccttc		3076
tagttgccag ccacatgttg tttgccccctc ccccgctgcct tccttgaccc tggaaagggtgc		3136
cactcccaact gtccttcct aataaaatga ggaaattgca tcgcattgtc tgtagtaggtg		3196
tcattctatt ctggggggtg ggggtggggca ggacagcaag gggggaggatt gggaaagacaa		3256
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attaatgaat cggccaaacgc gcggggagag gcggttgcg tattggcgc tcttccgctt		3376
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tatcaaaaag gatcttcacc	tagatcctt	taaattaaaa	atgaagttt	aatcaatct	4276
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ctacgatacg ggagggctta	ccatctggcc	ccagtgcgtc	aatgataccg	cgagacccac	4456
gctcaccggc tccagattta	tcagcaataa	accagccagc	cggaaggggc	gagcgcagaa	4516
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<210> 22

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<400> 22

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Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Leu	Gln	Leu	Ser	Thr	Tyr	Gln	Gly	
								20		25			30			
Lys	Val	Leu	Met	Ser	Ile	Asn	Lys	Thr	Asp	Ala	Gln	Ser	Ala	Ile	Asn	
							35		40			45				
Ile	Pro	Ser	Ala	Asn	Gly	Ala	Asn	Thr	Cys	Ile	Val	Arg	Ala	Leu	Asp	
							50		55			60				
Val	Gly	Val	Met	Cys	Lys	Asp	Asp	Ile	Thr	Tyr	Leu	Cys	Pro	Val	Leu	
							65		70		75		80			
Ser	Ala	Gly	Asn	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asp	Val	Glu		
							85		90			95				
Glu	Val	Trp	Val	His	Tyr	Gly	Arg	Cys	Thr	Arg	Met	Gly	His	Ser	Arg	
							100		105			110				
Arg	Ser	Arg	Arg	Ser	Ile	Ser	Val	Gln	His	His	Gly	Asp	Ser	Thr	Leu	
							115		120			125				
Ala	Thr	Lys	Asn	Thr	Pro	Trp	Leu	Asp	Thr	Val	Lys	Thr	Thr	Lys	Tyr	
							130		135			140				

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu  
 145 150 155 160  
 Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg  
 165 170 175  
 Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe  
 180 185 190  
 Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly  
 195 200 205  
 Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Ser Cys Val Thr Val  
 210 215 220  
 Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu  
 225 230 235 240  
 Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu  
 245 250 255  
 Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His  
 260 265 270  
 Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val  
 275 280 285  
 Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile  
 290 295 300  
 Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr  
 305 310 315 320  
 Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly  
 325 330 335  
 Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys  
 340 345 350  
 Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr  
 355 360 365  
 Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg  
 370 375 380  
 Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys  
 385 390 395 400  
 Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp  
 405 410 415  
 Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu  
 420 425 430  
 Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser  
 435 440 445  
 Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr  
 450 455 460  
 Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg  
 465 470 475 480  
 Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys  
 485 490 495  
 Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly  
 500 505 510  
 Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg  
 515 520 525  
 Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly  
 530 535 540  
 Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn  
 545 550 555 560  
 Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val  
 565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly  
 580 585 590  
 Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg  
 595 600 605  
 Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly  
 610 615 620  
 Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala  
 625 630 635 640  
 Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu  
 645 650 655  
 Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile  
 660 665 670  
 Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr  
 675 680 685  
 Ser Val Gln Ala  
 690

<210> 23  
 <211> 5271  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<221> CDS  
 <222> (910)...(2953)

<400> 23  
 gacggatcgg gagatctccc gatcccstat ggtcgactct cagtacaatc tgctctgatg 60  
 ccccatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120  
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatt aagaatctgc 180  
 ttagggtagt gcgtttgcg ctgcttcgcg atgtacgggc cagatatacg cggtgacatt 240  
 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300  
 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaaacgacc 360  
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420  
 attgacgtca atgggtggac tatttacggt aaactgccc cttggcagta catcaagtgt 480  
 atccatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540  
 atgcccagta catgaccta tggacttcc ctacttggca gtacatctac gtattagtca 600  
 tcgctattac catggtgatg cgggtttggc agtacatcaa tggcggttgc tagcggtttg 660  
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tggagtttgc ttttggcacc 720  
 aaaatcaacg ggacttcca aaatgtcgta acaactccgc cccattgacg caaatggcg 780  
 gtaggcgtgt acgggtggag gtctatataa gcagagctct ctggcttaact agagaaccca 840  
 ctgcttactg gcttatcgaa attaatacgat ctcactatag ggagacccaa gcttggtacc 900  
 gccgcccgc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951  
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser  
 1 5 10

ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999  
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys  
 15 20 25 30

aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047

Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr				
35	40	45		
ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag				1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys				
50	55	60		
tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca				1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro				
65	70	75		
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac				1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn				
80	85	90		
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg				1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg				
95	100	105	110	
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag				1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys				
115	120	125		
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc				1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu				
130	135	140		
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg				1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr				
145	150	155		
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc				1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val				
160	165	170		
gtg att gcc cta ctg gtc ttg gct ggt ccg gcc tac tca gct cac				1479
Val Ile Ala Leu Leu Val Ala Val Gly Pro Ala Tyr Ser Ala His				
175	180	185	190	
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga				1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly				
195	200	205		
act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg				1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met				
210	215	220		
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att				1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile				
225	230	235		
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act				1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr				
240	245	250		

cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta		1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu		
255	260	265
270		
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat		1767
Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp		
275	280	285
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg		1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val		
290	295	300
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt		1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val		
305	310	315
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg		1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly		
320	325	330
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat		1959
Ala Lys Gln Glu Asn Trp Thr Asp Ile Lys Thr Leu Lys Phe Asp		
335	340	345
350		
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct		2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala		
355	360	365
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac		2055
Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr		
370	375	380
atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc		2103
Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala		
385	390	395
cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga		2151
Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Val Trp Arg		
400	405	410
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc		2199
Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile		
415	420	425
430		
aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt		2247
Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu		
435	440	445
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac		2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr		
450	455	460
aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg		2343

Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu  
 465 470 475

aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt 2391  
 Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe  
 480 485 490

gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg 2439  
 Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val  
 495 500 505 510

aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat 2487  
 Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp  
 515 520 525

gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc 2535  
 Asp Leu Thr Ala Ala Asn Lys Gly Ile Leu Val Thr Val Asn Pro  
 530 535 540

atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct 2583  
 Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro  
 545 550 555

ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act 2631  
 Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr  
 560 565 570

tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag 2679  
 Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln  
 575 580 585 590

acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg 2727  
 Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp  
 595 600 605

gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att 2775  
 Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile  
 610 615 620

cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac 2823  
 His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn  
 625 630 635

tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc 2871  
 Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile  
 640 645 650

aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg 2919  
 Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val  
 655 660 665 670

atc atg atg ttt ttg tct cta gga gtt ggg gcg t gagcggccgc 2963  
 Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala  
 675 680

tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaaatgctag agctcgctga 3023  
 tcagcctcga ctgtgccttc tagttgccag ccacatgttg tttgccccctc cccccgtgcct 3083  
 tccttgaccc tggaaagggtc cactcccact gtcctttcct aataaaaatga ggaaattgca 3143  
 tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag 3203  
 ggggaggatt gggaaagacaa tagcaggcat gctggggatg cgggtggctc tatggcttct 3263  
 gaggcgaaa gaacagctgc attaatgaat cggccaacgc gcggggagag gcgggttgcg 3323  
 tattggcgcc tcttcgcctt cctcgctcac tgactcgctg cgctcgctcg ttccggctgcg 3383  
 gcgagcggta tcagctcact caaaggcggt aatacggtta tccacagaat cagggataa 3443  
 cgccaggaaag aacatgtgag caaaaggcca gcaaaaaggcc aggaaccgta aaaaggccgc 3503  
 gttgctggcg tttttccata ggctccgccc cccctgacgag catcacaaaa atcgacgctc 3563  
 aagtcaaggg tggcgaaacc cgacaggact ataaagatac caggcggttc cccctggaaag 3623  
 ctcccctcggt cgcttcgcctt ttccgacccct gccgcttacc ggataacctgt ccgcctttct 3683  
 cccttcggga agcgtggcgc tttctcaatg ctcacgctgt aggtatctca gttcgggtgt 3743  
 ggtcggtcgc tccaaagctgg gctgtgtca cgaacccccc gttcagcccg accgctgcgc 3803  
 cttatccggta aactatcgtc ttgagtc当地 cccggtaaga cacgacttat cgccactggc 3863  
 agcagccact ggtaacacgga ttagcagagc gaggtatgtt ggcgggtgcta cagagttctt 3923  
 gaagtgggtgg cctaaactacg gctacactag aaggacagta tttggtatct ggcctctgt 3983  
 gaagccagtt accttcggaa aaagagtgg tagctcttga tccggcaaaac aaaccaccgc 4043  
 tggtagcggt ggttttttgg tttgcaagca gcagattacg cgccggaaaggatctca 4103  
 agaagatccct ttgatctttt ctacggggcgc tgacgctcag tggaaacgaaa actcacgtta 4163  
 agggatttttgg gtcatgagat tatcaaaaag gatcttcacc tagatcctt taaaattaaaa 4223  
 atgaagttttt aaatcaatct aaagtatata tgagtaaact tggctctgaca gtacccaatg 4283  
 cttaatcagt gaggcaccta tctcagcgtat ctgtcttattt cggtcatcca tagttgcctg 4343  
 actccccgtc gtgtagataa ctacgatacg ggagggttta ccatctggcc ccagtgcgtc 4403  
 aatgataccg cgagacccac gctcaccggc tccagattta tcagcaataa accagccagc 4463  
 cggaaaggccg gggcgagaa gtggctctgc aactttatcc gctccatcc agtctattaa 4523  
 ttgttgc当地 ggagctagag taagtagttc gccagttaaat agtttgc当地 acgttgggtc 4583  
 cattgctaca ggcacatcggtt gtcacgctc gtgtttggat atggcttcat tcagctccgg 4643  
 ttcccaacga tcaaggcgag ttacatgatc cccatgttg tgcaaaaaag cggttagctc 4703  
 ctccggcctt ccgatcggtt tcagaagataa gttggccgca gtgttatcactcatggttat 4763  
 ggcagcactg cataattctc ttactgtcat gccatccgtt agatgtttt ctgtgactgg 4823  
 tgagtactca accaagtcat tctgagaata gtgtatgc当地 cgaccgagtt gctcttgc当地 4883  
 ggcgtcaata cgggataata ccgc当地 caca tagcagaact taaaatgc当地 tcatcattgg 4943  
 aaaaacgttct tcggggcgaa aactctcaag gatcttaccg ctgttggat ccagttcgat 5003  
 gtaacccact cgtgcaccca actgatcttc agcatctttt actttcacca gctttctgg 5063  
 gtgagcaaaa acaggaaggc aaaatgc当地 aaaaaggaa ataaggcgaa cacggaaatg 5123  
 ttgaataactc atactcttcc ttttcaata ttattgaagc atttatcagg gttattgtct 5183  
 catgagcgga tacatatttgg aatgttattta gaaaaataaaa caaataagggg ttccgc当地 5243  
 atttccccgaa aaagtgc当地 ctgacgctc 5271

<210> 24  
 <211> 681  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of artificial sequence; note =  
 synthetic construct

<400> 24  
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
 1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg  
20 25 30  
Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser  
35 40 45  
Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp  
50 55 60  
Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu  
65 70 75 80  
Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg  
85 90 95  
Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg  
100 105 110  
Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg  
115 120 125  
Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys  
130 135 140  
Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu  
145 150 155 160  
Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile  
165 170 175  
Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile  
180 185 190  
Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp  
195 200 205  
Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro  
210 215 220  
Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg  
225 230 235 240  
Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val  
245 250 255  
Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu  
260 265 270  
Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly  
275 280 285  
Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys  
290 295 300  
Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln  
305 310 315 320  
Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys  
325 330 335  
Gln Glu Asn Trp Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu  
340 345 350  
Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu  
355 360 365  
Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala  
370 375 380  
Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp  
385 390 395 400  
Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met  
405 410 415  
His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val  
420 425 430  
Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly  
435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu  
 450 455 460  
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu  
 465 470 475 480  
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys  
 485 490 495  
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val  
 500 505 510  
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu  
 515 520 525  
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala  
 530 535 540  
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly  
 545 550 555 560  
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln  
 565 570 575  
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met  
 580 585 590  
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe  
 595 600 605  
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr  
 610 615 620  
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile  
 625 630 635 640  
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr  
 645 650 655  
 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met  
 660 665 670  
 Met Phe Leu Ser Leu Gly Val Gly Ala  
 675 680

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature

<222> 1-35

<223> POW 454

<400> 25

aaaagaaaaaa gcgctaccac catccaccgg gacag

35

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-41  
<223> CPOW 2417

<400> 26  
actgttaccc tcaaccccg actcgccggc gaaaaagaaa a 41

<210> 27  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<223> Modified JE Signal

<400> 27  
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala  
1 5 10 15  
Val Val Ile Ala Gly Thr Ser Ala  
20

<210> 28  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 1-36  
<223> YF 482

<400> 28  
aaaaagaaaaa gcgctgtgac cttggcgg aaaaac 36

<210> 29  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature

<222> 1-41

<223> CYF 2433

<400> 29

acagagatcc tcaaccccgcc actcgccggc gaaaaagaaaa a

41

<210> 30

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature

<222> 1-41

<223> SLE 463

<400> 30

aaaagaaaaaa gcgcgttgca gttatcaacc tatcagggga a

41

<210> 31

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =  
synthetic construct

<221> misc\_feature

<222> 1-40

<223> CSLE 2477

<400> 31

accgttggtc gcacgttcgg actcgccggc gaaaaagaaaa

40